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HERITABILITY OF GROWTH TRAITS FOR SMALL ABALONE *HALIOTIS DIVERSICOLOR* ESTIMATED FROM SIB MATINGS

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ABSTRACT Twelve half-sib groups and 36 full-sib groups of small abalone *Haliotis diversicolor* were obtained by the unbalanced nest design using artificial fertilization of 3 females by each male. Heritabilities of growth-related traits were estimated from postlarva to market size at days 10, 40, 120, 220, 320, and 420. The estimated heritabilities based on sire components for shell length and shell width were 0.15 – 0.37 and 0.18 – 0.42, respectively. Heritability estimate for shell length and shell width based on dam component were larger than those based on sire component. The results in the current study indicate that genetic improvement through selective breeding conducted on small abalone might be available and would be an efficient method to obtain a positive response to selection.

KEY WORDS: abalone, *Haliotis diversicolor,* heritability, growth, half-sib

INTRODUCTION

Heritability, genetic correlation, and repeatability are the 3 most important parameters in animal breeding research. Heritability, which measures the relative magnitude of additive genetic variation, indicates the proportion of total phenotypic variation that is genetic in origin (Falconer & Mackay 1996). Reliable estimates of genetic parameters can provide valuable information for determining reasonable breeding plans and predicting selection response of candidate traits (Wang et al. 2006a). Henderson's (1973) technique, which enables one to separate genetic and environmental effects when predicting animal breeding values, is broadly used to estimate heritability in animal breeding projects. Most published estimates of heritability in shellfish species have been calculated by regression of response on selection differentials (Heffernan et al. 1991, Jarayabhand & Thavornyutikarn 1995, Ibarra et al. 1999). Recently, nested analysis of the variance model has begun to be used for heritability estimating in aquatic animal breeding (Wang et al. 2006a, Liu et al. 2005, Wang et al. 2006b).

China is the most important abalone-producing country in the world (Roberto & Gutierrez 2007). Small abalone *Haliotis diversicolor* is naturally distributed along the coastal waters of East Asia and is a commercially important species cultured along the coast of southern China and Taiwan (Cai & Wang 2008). It has a short grow-out period and can grow to market size (55–70 mm in shell length) in 10–12 mo. Commercial seed production of small abalone in China was begun in 1992, when this species was introduced from Taiwan to the southern China coasts. However, since late 2000, the lack of selective breeding practices has resulted in a decrease in growth rate. Increasing the growth rate of abalone through selective breeding is becoming important in terms of viability of the industry and is a priority for growers (Viana 2002). Genetic breeding and improvement programs for small abalone have been established in China since 2003.

The first study about heritability for growth traits in abalone species by nested design was conducted in red abalone *H. rufescens* in Iceland (Jonasson et al. 1999). One hundred families were established using a hierarchical mating system of 1 male to 2–6 females. Heritability estimates for shell length at 8, 10, 18, and 24 mo of age are 0.08, 0.06, 0.27, and 0.34, respectively. In another study, heritability for growth- related traits of tropical abalone donkey's ear abalone *H. asinina* was estimated by creating a single cohort of 84 families in a full-factorial mating design (Lucas et al. 2006). Heritability estimates were 0.48 ± 0.15 for shell length, 0.38 ± 0.13 for shell width, and 0.36 ± 0.13 for weight. Deng et al. (2007) showed that heritability ranged from 0.23–0.36 for shell length and 0.21–0.32 for shell width in the Pacific abalone *H. discus hannai* Ino from 12 half-sib families and 36 full-sib families at 10, 20, and 30 days after fertilization. These experiments suggest that growth traits could be improved through selection in abalone.

In the current study, heritabilities of growth-related traits for small abalone were estimated by the unbalanced nest design using artificial fertilization of 3 females for each male. The results will be useful for selective breeding projects of small abalone.

MATERIALS AND METHODS

Experimental Animals and Broodstock Conditioning

Small, mature male abalone from a Japanese population and small female abalone from a Taiwanese population were used as broodstock to build the cross-line in 2005; cross-bred offspring were cultured at Dongshan Haitian Aquaculture Co., Ltd., Fujian Province (You et al. 2009). One hundred cross-bred progeny were collected as broodstock for this research in 2007 and were cultured in a multiple-tier basket system (Chen & Lee 1999). The abalone were fed in excess with a macroalga *Gracilaria* sp. Water temperature was kept at 26–28°C. The abalone reached ripeness as visually determined according to Yang et al. (1975).

Spawning, Fertilization, and Establishment of Families

Males and females were induced to spawn utilizing stimulation by ultraviolet-irradiated seawater and temperature shock (Kikuchi & Uki 1974). The eggs of each of 3 females were

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TABLE 1.

Mean, SD, and coefficient of variation (CV) for shell length and shell width at the early juvenile and later juvenile stages.

Age (days)	Family No.	Sample No.	Shell Length (mm)		Shell Width (mm)	
			Mean ± SD	CV	Mean ± SD	CV
10	36	1,080	0.53 ± 0.13	24.5%	0.33 ± 0.05	15.1%
40	36	1,080	3.05 ± 0.96	31.5%	1.94 ± 0.39	20.1%
120	34	1,020	11.23 ± 3.74	33.3%	7.22 ± 1.86	25.8%
220	32	960	25.36 ± 6.86	27.1%	16.21 ± 4.12	25.4%

fertilized with sperm from 1 male. The released sperm from 1 male and about 100,000 eggs from each female were mixed for insemination, and then fertilized eggs were washed 3 times in 0.22-mm filtered seawater to remove excessive sperm. Fertilized eggs hatched into veliger larvae about 9 h after fertilization in seawater at a temperature of 26°C and a salinity of 30 ± 1. Larvae were then placed into 500-L fiber reinforced plastic tanks to establish a full-sib family. Eight plastic plates (60 × 40 cm), coated with benthic diatoms served, as cue for postlarval settlement and were suspended in each tank.

This study was conducted based on the classic nested mating design by Comstock and Robinson (1952). In our experiment, each of 12 males was mated to an average of 3 females, generating 36 full-sib families and 12 sets of half-sib families. Variance components for each trait were estimated using a simple variance component estimation procedure (Gall & Bakar 2002), whereas covariance components for pairs of traits were estimated using a simple random model.

Early Juvenile, Later Juvenile, and Grow-out Rearing

Larval rearing conditions, such as water temperature, salinity, light intensity, and the initial larval density were maintained the same for all 36 families. The initial larval density was 0.2/mL. Three to 4 days after fertilization, free-swimming larvae began the process of settlement and metamorphosis, and then transferred into early juveniles, which fed on the diatoms on the plastic plates.

The early juveniles reached 2–4 mm after 40 days of rearing on the plastic plates and were then peeled off onto cement bricks, under which juvenile abalone could shelter from the light during daytime. Abalone then transferred into the later juvenile stage. The density of later juveniles was adjusted to 1,200 individuals per tank (tank size, 1.2 × 0.6 × 0.7 m; water volume, 500 L). Thin *Gracilaria* sp. and an artificial feed were used as food. Excrement and remaining feed were siphoned off every 2 days.

After 4 mo, later juveniles grew to about 20 mm and were transported into baskets (40 × 30 × 12 cm) for field grow-out. The initial density was 20 individuals to each basket, and *Gracilaria* sp. was used as food for the small abalone. During initial growth, all individuals in the same family were mixed every month during maintenance and were randomly redistributed in the baskets. During the early juvenile, later juvenile, and grow-out stages, no individual was discarded intentionally.

Sampling and Measurement

Shell length and shell width of 30 individuals per family were randomly measured on days 10, 40, 120, 220, 320, and 420. During the grow-out stage, the body weight of each family was measured at day 320 and day 420. Shell length was measured using a microscope equipped with an ocular micrometer or vernier caliper (0.02-mm accuracy). Body weight was measured using an electronic balance (0.01-g accuracy).

Statistical Analysis

Phenotypic variance was decomposed into genetic and environmental components of variance through the covariance among full- and half-sibs. The covariance was calculated from the observed components of variance obtained from the General Linear Models procedure in the Statistical Analysis System (Freund et al. 1986) based on the random nested design model (Liu et al. 2005, Wang et al. 2006a):

$$Y_{ijk} = \mu + s_i + d_{ji} + e_{ijk}$$

where Y_{ijk} is the variable studied for individual k in the full-sib family from dam j and sire i, μ is the overall mean, s_i is the random effect of sire i, d_{ji} is the random effect of dams j within sire i, and e_{ijk} is the random residual.

Sire heritability was estimated as $h_s^2 = 4\sigma_s^2/(\sigma_s^2+\sigma_d^2+\sigma_e^2)$, dam heritability was estimated as $h_d^2 = 4\sigma_d^2/(\sigma_s^2+\sigma_d^2+\sigma_e^2)$, and combined (sire and dam) heritability was estimated as $h^2_{s+d} = 2(\sigma_s^2+\sigma_d^2)/(\sigma_s^2+\sigma_d^2+\sigma_e^2)$. Heritabilities were tested at a significance of $t = h_d^2/\sigma_h$. The standard errors of heritability was estimated as in Becker (1984).

RESULTS

Mean, SD, and coefficients of variation for shell length, shell width, and body weight at different age stages are listed in Tables 1 and 2. Because of high mortality in some families during the culture period, several families were discarded. Therefore, 34 families at day 120, 32 families at day 220, 30 families at day 320, and 28 families at day 420 were measured. For shell length and shell width, coefficients were lower at the grow-out stage compared with the early and later juvenile

TABLE 2.

Mean, SD, and coefficient of variation (CV) for shell length, shell width, and body weight at grow-out stages.

Age (days)	Family No.	Sample No.	Shell Length (mm)		Shell Width (mm)		Body Weight (g)	
			Mean ± SD	CV	Mean ± SD	CV	Mean ± SD	CV
320	30	900	49.55 ± 8.97	18.1%	31.76 ± 5.05	15.9%	15.63 ± 3.78	24.2%
420	28	840	57.63 ± 10.21	17.7%	37.24 ± 5.51	14.8%	20.89 ± 6.89	32.9%

TABLE 3.

Heritability of shell length and shell width at the early juvenile and later juvenile stages (h^2 ± SD).

Age (days)	Source	Shell Length	Shell Width
10	Sire	0.37 ± 0.05	0.42 ± 0.04
	Dam	0.46 ± 0.07	0.51 ± 0.04
	Combined	0.42 ± 0.05	0.45 ± 0.05
40	Sire	0.28 ± 0.04	0.31 ± 0.05
	Dam	0.36 ± 0.06	0.40 ± 0.06
	Combined	0.31 ± 0.05	0.33 ± 0.05
120	Sire	0.15 ± 0.08	0.18 ± 0.08
	Dam	0.27 ± 0.09	0.29 ± 0.05
	Combined	0.22 ± 0.08	0.24 ± 0.07
220	Sire	0.19 ± 0.07	0.19 ± 0.04
	Dam	0.32 ± 0.06	0.32 ± 0.06
	Combined	0.25 ± 0.06	0.26 ± 0.05

TABLE 4.

Heritability of shell length, shell width, and body weight at grow-out stages (h^2 ± SD).

Age (days)	Source	Shell Length	Shell Width	Body Weight
320	Sire	0.23 ± 0.07	0.27 ± 0.05	0.34 ± 0.05
	Dam	0.33 ± 0.07	0.31 ± 0.07	0.46 ± 0.05
	Combined	0.26 ± 0.07	0.28 ± 0.06	0.38 ± 0.05
420	Sire	0.21 ± 0.06	0.23 ± 0.06	0.27 ± 0.05
	Dam	0.24 ± 0.05	0.29 ± 0.05	0.35 ± 0.05
	Combined	0.23 ± 0.05	0.25 ± 0.04	0.29 ± 0.05

stages. The coefficient was highest for body weight (24.2% and 32.9%) compared with shell length (18.1% and 17.7%) and shell width (15.9% and 14.8%) at days 320 and 420.

All heritability estimates (Tables 3 and 4) for shell length, shell width, and body weight at different age were significantly different from 0 ($P < 0.01$). According to the results, moderate heritabilities were observed. The estimated heritabilities based on sire components for shell length and shell width from day 10 to day 420 were 0.15–0.37 and 0.18–0.42, respectively. All the heritabilities estimated from dam components were higher than those estimated from sire components and combined components. The differences were indistinct between the estimated heritabilities from sire components and combined components.

Heritabilities of shell width were usually slightly higher than the values of shell length. However, heritability estimates of body weight were higher than the values of both shell length and shell width at day 320 and day 420.

DISCUSSION

Generally, the half-sib correlation and the regression of offspring on sire are the most reliable ways to estimate heritability. Full-sib correlation is the least reliable, because they are influenced by common environmental effects and dominance variance (Gjedrem 2005). In this research, the estimated heritabilities from sire components for growth-related traits in small abalone were moderate to high—0.15–0.37 for shell length and 0.18–0.42 for shell width—which was higher than the results of red abalone *H. rufescens* (Jonasson et al. 1999), lower than the results of donkey's ear abalone *H. asinina* (Lucas et al. 2006), and similar to the results of Pacific abalone *H. discus hannai* (Deng et al. 2007). The moderate to high estimated heritabilities of small abalone indicated significant additive genetic variation for body weight and morphological traits at all sampling periods. These results show that it is possible to increase the body weight and growth-related traits when selection is applied.

It is common that the evaluated heritabilities based on the sire component were low in contrast to dam components. The same results were found in small abalone. The nonadditive genetic effects, dominance effect, maternal effect, additive-by-additive interaction effect, and environment effect in full-sib design may induce bias in evaluated variances (Blanc 2003). The presence of significant maternal effects was observed in our experiment. Crandell and Gall (1993) reported that dam effects can persist as long as to 2 y in rainbow trout.

Realized heritability of shell length for small abalone has been calculated by regression of response on selection differentials in a divergent selection experiment (You et al. 2009). The average realized heritability for shell length was 0.441 ± 0.064 and 0.113 ± 0.013 for 2 stocks with a different genetic background. Compared with realized heritability, the moderate level of heritability in this research is acceptable. However, it should be realized that heritability is not a static characteristic of a breeding population. It is only relevant to the data used for estimation, or the population from which the data were sampled. When environmental conditions are changed, the heritability may change (Gjedrem 2005).

In this study, moderate to high heritability of growth-related traits was estimated for small abalone at different growing stages. The results indicate that selection of body weight and morphological traits could result in a positive response and would be feasible in a genetic breeding program of small abalone.

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